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#3

SEQUENCE LISTING

<110> NAGATA, Shigekazu et al

<120> DNA CODING FOR HUMAN CELL SURFACE ANTIGEN

<130> 0020-4877P

<140> US 09/884,987
<141> 2001-06-21

<160> 11

<170> PatentIn version 3.0

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ctcccgcggg ttggtggacc cgctcagtac ggagttgggg aagctctttc acttcggagg 180

attgctcaac aacc atg ctg ggc atc tgg acc ctc cta cct ctg gtt ctt 230
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Thr Ser Val Ala Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr

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Asp Ile Asn Ser Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val
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gag act cag aac ttg gaa ggc ctg cat cat gat ggc caa ttc tgc cat      374
Glu Thr Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His
    30                  35                  40

aag ccc tgt cct cca ggt gaa agg aaa gct agg gac tgc aca gtc aat      422
Lys Pro Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn
45                  50                  55                  60

ggg gat gaa cca gac tgc gtg ccc tgc caa gaa ggg aag gag tac aca      470
Gly Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr
                65                  70                  75

gac aaa gcc cat ttt tct tcc aaa tgc aga aga tgt aga ttg tgt gat      518
Asp Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp
            80                  85                  90

gaa gga cat ggc tta gaa gtg gaa ata aac tgc acc cgg acc cag aat      566
Glu Gly His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn
        95                  100                 105

acc aag tgc aga tgt aaa cca aac ttt ttt tgt aac tct act gta tgt      614
Thr Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys
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gaa cac tgt gac cct tgc acc aaa tgt gaa cat gga atc atc aag gaa      662
Glu His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu
125                 130                 135                 140

tgc aca ctc acc agc aac acc aag tgc aaa gag gaa gga tcc aga tct      710
Cys Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser
                145                 150                 155

aac ttg ggg tgg ctt tgt ctt ctt ctt ttg cca att cca cta att gtt      758
Asn Leu Gly Trp Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val
            160                 165                 170

tgg gtg aag aga aag gaa gta cag aaa aca tgc aga aag cac aga aag      806
Trp Val Lys Arg Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys
        175                 180                 185

gaa aac caa ggt tct cat gaa tct cca acc tta aat cct gaa aca gtg      854
Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val
    190                 195                 200

gca ata aat tta tct gat gtt gac ttg agt aaa tat atc acc act att      902
Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile
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gct gga gtc atg aca cta agt caa gtt aaa ggc ttt gtt cga aag aat      950
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Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln
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gac aca gca gaa cag aaa gtt caa ctg ctt cgt aat tgg cat caa ctt     1046
Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu
        255                 260                 265

cat gga aag aaa gaa gcg tat gac aca ttg att aaa gat ctc aaa aaa     1094
His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys
    270                 275                 280

gcc aat ctt tgt act ctt gca gag aaa att cag act atc atc ctc aag     1142
Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys
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gac att act agt gac tca gaa aat tca aac ttc aga aat gaa atc caa     1190
Asp Ile Thr Ser Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln
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Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
20 25 30

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
35 40 45

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
50 55 60

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
65 70 75 80

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
85 90 95

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
100 105 110

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
115 120 125

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr

130 135 140

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
145 150 155 160

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
165 170 175

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
180 185 190

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu
195 200 205

Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met
210 215 220

Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu
225 230 235 240

Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu
245 250 255

Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys
260 265 270

Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys
275 280 285

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Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
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Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys
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    50                  55                  60

His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys
65                  70                  75                  80

Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His
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Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
        35                  40                  45

Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg
    50                  55                  60

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp
65                  70                  75                  80

Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu
                85                  90                  95

Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val
            100                 105                 110

His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala
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Lys Ser Leu Glu Cys Thr Lys Leu Cys
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Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
35 40 45

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Asp
50 55 60

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
65 70 75 80

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
85 90 95

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
100 105 110

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
115 120 125

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
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Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
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Val Cys Thr

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Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr
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Val Cys Glu Pro Cys Leu Asp Ser Val Thr Ser Ser Asp Val Val Ser
35 40 45

Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser
50 55 60

Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala
65 70 75 80

Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg
85 90 95

Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln
100 105 110

Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala
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Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu
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20 25 30

Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe Leu Asp Thr Trp Asn
35 40 45

Arg Glu Thr His Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly
50 55 60

Leu Arg Val Gln Gln Lys Gly Thr Ser Glu Thr Asp Thr Ile Cys Thr
65 70 75 80

Cys Glu Glu Gly Trp His Cys Thr Ser Glu Ala Cys Glu Ser Cys Val
85 90 95

Leu His Arg Ser Cys Ser Pro Gly Phe Gly Val Lys Gln Ile Ala Thr
100 105 110

Gly Val Ser Asp Thr Ile Cys Glu Pro Cys Pro Val Gly Phe Phe Ser
115 120 125

Asn Val Ser Ser Ala Phe Glu Lys Cys His Pro Thr Ser Cys Glu Thr
130 135 140

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Cys Gly

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Thr Val Cys His Asn Cys Val Lys Asp Thr Tyr Pro Ser Gly His Lys
35 40 45

Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val Ser Arg Cys Asp
50 55 60

His Thr Arg Asp Thr Val Cys His Cys Arg Pro Gly Thr Gln Pro Arg
65 70 75 80

Gln Asp Ser Ser His Lys Phe Gly Val Asp Cys Val Pro Cys Pro Pro
85 90 95

Gly His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn
100 105 110

Cys Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Leu
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Asp Thr Val Cys Glu
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20 25 30

Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser
35 40 45